



RAW SEQUENCE LISTING

DATE: 10/01/2002

PATENT APPLICATION: US/10/089,678

TIME: 18:59:09

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF4\10012002\J089678.raw

3 <110> APPLICANT: ASANO, Shinichiro
 5 <120> TITLE OF INVENTION: PROTEIN HAVING INSECTICIDAL ACTIVITY, DNA ENCODING THE
 PROTEIN, AND

6 NOXIOUS ORGANISM-CONTROLLING AGENT AND METHOD

8 <130> FILE REFERENCE: Q68821

10 <140> CURRENT APPLICATION NUMBER: 10/089,678

11 <141> CURRENT FILING DATE: 2002-04-03

13 <150> PRIOR APPLICATION NUMBER: JP 2000-236140

14 <151> PRIOR FILING DATE: 2000-08-03

16 <150> PRIOR APPLICATION NUMBER: PCT/JP01/06660

17 <151> PRIOR FILING DATE: 2001-08-02

19 <160> NUMBER OF SEQ ID NOS: 3

21 <170> SOFTWARE: PatentIn version 3.1

23 <210> SEQ ID NO: 1

24 <211> LENGTH: 1167

25 <212> TYPE: PRT

26 <213> ORGANISM: Bacillus thuringiensis

28 <400> SEQUENCE: 1

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 31 1 5 10 15
 34 Ser Thr Ser Val Ser Asp Asn Ser Val Arg Tyr Pro Leu Ala Asn Asp
 35 20 25 30
 38 Gln Thr Thr Thr Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Arg Met
 39 35 40 45
 42 Ser Glu Gly Glu Asn Pro Glu Leu Phe Gly Asn Pro Glu Thr Phe Ile
 43 50 55 60
 46 Ser Ser Ser Thr Val Gln Thr Gly Ile Gly Ile Val Gly Gln Val Leu
 47 65 70 75 80
 50 Gly Ala Leu Gly Val Pro Phe Ala Gly Gln Ile Ala Ser Phe Tyr Ser
 51 85 90 95
 54 Phe Ile Val Gly Gln Leu Trp Pro Ser Ser Thr Val Ser Val Trp Glu
 55 100 105 110
 58 Met Ile Met Lys Gln Val Glu Asp Leu Ile Asp Gln Lys Ile Thr Asp
 59 115 120 125
 62 Ser Val Arg Lys Thr Ala Leu Ala Gly Leu Gln Gly Leu Gly Asp Gly
 63 130 135 140
 66 Leu Asp Val Tyr Gln Lys Ser Leu Lys Asn Trp Leu Glu Asn Arg Asn
 67 145 150 155 160
 70 Asp Thr Arg Ala Arg Ser Val Val Val Thr Gln Tyr Ile Ala Leu Glu
 71 165 170 175
 74 Leu Asp Phe Val Ala Lys Ile Pro Ser Phe Ala Ile Ser Gly Gln Glu
 75 180 185 190
 78 Val Pro Leu Leu Ser Val Tyr Ala Gln Ala Ala Asn Leu His Leu Leu
 79 195 200 205

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82 Leu Leu Arg Asp Ala Ser Ile Phe Gly Ala Glu Trp Gly Phe Thr Pro
83      210      215      220
86 Gly Glu Ile Ser Thr Phe Tyr Asp Arg Gln Val Thr Arg Thr Ala Gln
87 225      230      235      240
90 Tyr Ser Asp Tyr Cys Val Lys Trp Tyr Asn Thr Gly Leu Asp Lys Leu
91      245      250      255
94 Lys Gly Thr Asn Ala Ala Ser Trp Leu Lys Tyr His Gln Phe Arg Arg
95      260      265      270
98 Glu Met Thr Leu Leu Val Leu Asp Leu Val Ala Leu Phe Pro Asn Tyr
99      275      280      285
102 Asp Thr Arg Thr Tyr Pro Ile Glu Thr Thr Ala Gln Leu Thr Arg Glu
103      290      295      300
106 Val Tyr Thr Asp Pro Ile Val Phe Asn Arg Glu Thr Ser Gly Gly Phe
107 305      310      315      320
110 Cys Arg Arg Trp Ser Leu Asn Ser Asp Ile Ser Phe Ser Glu Val Glu
111      325      330      335
114 Ser Ala Val Ile Arg Ser Pro His Leu Phe Asp Ile Leu Ser Glu Ile
115      340      345      350
118 Glu Phe Tyr Thr Thr Arg Ala Gly Leu Pro Leu Asn Asn Thr Glu Tyr
119      355      360      365
122 Leu Glu Tyr Trp Val Gly His Ser Ile Lys Tyr Lys Asn Thr Asn Ala
123      370      375      380
126 Ser Ser Ala Leu Glu Arg Asn Tyr Gly Thr Ile Thr Ser Asn Lys Ile
127 385      390      395      400
130 Lys Tyr Tyr Asp Leu Ala Asn Lys Asp Ile Phe Gln Val Arg Ser Leu
131      405      410      415
134 Gly Ala Asp Leu Ala Asn Tyr Tyr Ala Gln Val Tyr Gly Val Pro Tyr
135      420      425      430
138 Ala Ser Phe Thr Leu Leu Asp Lys Asn Thr Gly Ser Gly Ser Val Gly
139      435      440      445
142 Gly Phe Thr Tyr Ser Lys Pro His Thr Thr Met Gln Val Cys Thr Gln
143      450      455      460
146 Asn Tyr Asn Thr Ile Asp Glu Ile Pro Pro Glu Asn Glu Pro Leu Ser
147 465      470      475      480
150 Arg Gly Tyr Ser His Arg Leu Ser His Ile Thr Ser Tyr Ser Phe Ser
151      485      490      495
154 Lys Asn Ala Ser Ser Pro Ala Arg Tyr Gly Asn Leu Pro Val Phe Ala
155      500      505      510
158 Trp Thr His Arg Ser Ala Asp Val Thr Asn Thr Val Tyr Ser Asp Lys
159      515      520      525
162 Ile Thr Gln Ile Pro Val Val Lys Ala His Thr Leu Val Ser Gly Thr
163      530      535      540
166 Thr Val Ile Lys Gly Pro Gly Phe Thr Gly Gly Asn Ile Leu Lys Arg
167 545      550      555      560
170 Thr Ser Ser Gly Pro Leu Ala Tyr Thr Ser Val Ser Val Lys Ser Pro
171      565      570      575
174 Leu Ser Gln Arg Tyr Arg Ala Arg Ile Arg Tyr Ala Ser Thr Thr Asn
175      580      585      590
178 Leu Arg Leu Phe Val Thr Ile Ser Gly Thr Arg Ile Tyr Ser Ile Asn

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278 Ser Ile Pro Tyr Val Tyr Asn Asp Ala Leu Pro Glu Ile Pro Gly Met
279      995      1000      1005
282 Asn Tyr Thr Ser Phe Thr Glu Leu Thr Asn Arg Leu Gln Gln Ala
283      1010      1015      1020
286 Trp Asn Leu Tyr Asp Leu Arg Asn Ala Ile Pro Asn Gly Asp Phe
287      1025      1030      1035
290 Arg Asn Gly Leu Ser Asp Trp Asn Ala Thr Ser Asp Val Asn Val
291      1040      1045      1050
294 Gln Gln Leu Ser Asp Thr Ser Val Leu Val Ile Pro Asn Trp Asn
295      1055      1060      1065
298 Ser Gln Val Ser Gln Gln Phe Thr Val Gln Pro Asn Tyr Arg Tyr
299      1070      1075      1080
302 Val Leu Arg Val Thr Ala Arg Lys Glu Gly Val Gly Asp Gly Tyr
303      1085      1090      1095
306 Val Ile Ile Arg Asp Gly Ala Asn Gln Thr Glu Thr Leu Thr Phe
307      1100      1105      1110
310 Asn Ile Cys Asp Asp Asp Thr Gly Val Leu Ser Ala Asp Gln Thr
311      1115      1120      1125
314 Ser Tyr Ile Thr Lys Thr Val Glu Phe Thr Pro Ser Thr Glu Gln
315      1130      1135      1140
318 Val Trp Ile Asp Met Ser Glu Thr Glu Gly Val Phe Asn Ile Glu
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323      1160      1165
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327 <211> LENGTH: 3504
328 <212> TYPE: DNA
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332 <221> NAME/KEY: exon
333 <222> LOCATION: (1)..(3501)
334 <223> OTHER INFORMATION:
337 <400> SEQUENCE: 2
338 atg agt cca aat aat caa aat gaa tat gaa att cta gat gct tca tca      48
339 Met Ser Pro Asn Asn Gln Asn Glu Tyr Glu Ile Leu Asp Ala Ser Ser
340 1      5      10      15
342 tct act tct gta tcc gat aat tct gtt aga tac cct tta gca aac gat      96
343 Ser Thr Ser Val Ser Asp Asn Ser Val Arg Tyr Pro Leu Ala Asn Asp
344      20      25      30
346 caa acg acc aca tta caa aac atg aac tat aaa gat tat ctg aga atg      144
347 Gln Thr Thr Thr Leu Gln Asn Met Asn Tyr Lys Asp Tyr Leu Arg Met
348      35      40      45
350 tct gag gga gag aat cct gaa tta ttt gga aat ccg gag acg ttt att      192
351 Ser Glu Gly Glu Asn Pro Glu Leu Phe Gly Asn Pro Glu Thr Phe Ile
352      50      55      60
354 agt tca tct acg gtt caa act gga att ggc att gtt ggt caa gta ctg      240
355 Ser Ser Ser Thr Val Gln Thr Gly Ile Gly Ile Val Gly Gln Val Leu
356 65      70      75      80
358 ggg gct tta ggg gtt cca ttt gct gga cag ata gct agt ttt tat agt      288

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359	Gly	Ala	Leu	Gly	Val	Pro	Phe	Ala	Gly	Gln	Ile	Ala	Ser	Phe	Tyr	Ser	
360				85					90					95			
362	ttc	att	gtc	ggt	caa	tta	tgg	cca	tca	agt	acc	gtg	agt	gta	tgg	gaa	336
363	Phe	Ile	Val	Gly	Gln	Leu	Trp	Pro	Ser	Ser	Thr	Val	Ser	Val	Trp	Glu	
364				100					105					110			
366	atg	att	atg	aaa	caa	gtg	gaa	gat	cta	att	gat	caa	aaa	ata	aca	gat	384
367	Met	Ile	Met	Lys	Gln	Val	Glu	Asp	Leu	Ile	Asp	Gln	Lys	Ile	Thr	Asp	
368				115					120					125			
370	tct	gta	agg	aaa	aca	gcg	ctt	gca	gga	cta	caa	gga	tta	gga	gat	ggc	432
371	Ser	Val	Arg	Lys	Thr	Ala	Leu	Ala	Gly	Leu	Gln	Gly	Leu	Gly	Asp	Gly	
372			130						135					140			
374	tta	gac	gta	tat	cag	aaa	tca	ctt	aag	aat	tgg	ctg	gaa	aat	cgt	aat	480
375	Leu	Asp	Val	Tyr	Gln	Lys	Ser	Leu	Lys	Asn	Trp	Leu	Glu	Asn	Arg	Asn	
376	145					150					155					160	
378	gat	aca	aga	gct	aga	agt	gtt	gtg	gtg	acc	caa	tat	ata	gct	tta	gag	528
379	Asp	Thr	Arg	Ala	Arg	Ser	Val	Val	Val	Thr	Gln	Tyr	Ile	Ala	Leu	Glu	
380					165					170					175		
382	ctt	gat	ttt	gtt	gct	aaa	atc	cca	tct	ttt	gca	ata	tct	gga	cag	gaa	576
383	Leu	Asp	Phe	Val	Ala	Lys	Ile	Pro	Ser	Phe	Ala	Ile	Ser	Gly	Gln	Glu	
384				180						185				190			
386	gta	cca	tta	tta	tca	gtg	tat	gca	caa	gca	gcg	aat	tta	cat	ttg	cta	624
387	Val	Pro	Leu	Leu	Ser	Val	Tyr	Ala	Gln	Ala	Ala	Asn	Leu	His	Leu	Leu	
388				195					200					205			
390	tta	tta	cga	gat	gct	tcc	att	ttt	gga	gca	gag	tgg	gga	ttc	aca	cca	672
391	Leu	Leu	Arg	Asp	Ala	Ser	Ile	Phe	Gly	Ala	Glu	Trp	Gly	Phe	Thr	Pro	
392			210					215					220				
394	gga	gaa	att	tcc	aca	ttt	tat	gat	cgt	cag	gtg	aca	cgt	acc	gcc	caa	720
395	Gly	Glu	Ile	Ser	Thr	Phe	Tyr	Asp	Arg	Gln	Val	Thr	Arg	Thr	Ala	Gln	
396	225					230					235					240	
398	tac	tcg	gat	tat	tgt	gta	aag	tgg	tat	aac	act	ggc	tta	gat	aaa	tta	768
399	Tyr	Ser	Asp	Tyr	Cys	Val	Lys	Trp	Tyr	Asn	Thr	Gly	Leu	Asp	Lys	Leu	
400					245					250					255		
402	aaa	ggt	acg	aat	gct	gca	agt	tgg	ctg	aag	tat	cac	caa	ttc	cga	aga	816
403	Lys	Gly	Thr	Asn	Ala	Ala	Ser	Trp	Leu	Lys	Tyr	His	Gln	Phe	Arg	Arg	
404				260					265					270			
406	gaa	atg	aca	tta	ctg	gta	tta	gat	tta	gta	gcg	tta	ttt	cca	aac	tat	864
407	Glu	Met	Thr	Leu	Leu	Val	Leu	Asp	Leu	Val	Ala	Leu	Phe	Pro	Asn	Tyr	
408				275					280					285			
410	gac	aca	cgt	acg	tat	cca	atc	gaa	aca	acg	gcc	caa	ctt	aca	cgg	gaa	912
411	Asp	Thr	Arg	Thr	Tyr	Pro	Ile	Glu	Thr	Thr	Ala	Gln	Leu	Thr	Arg	Glu	
412			290					295				300					
414	gtg	tat	aca	gat	cca	ata	gta	ttt	aac	aga	gaa	aca	agt	ggt	gga	ttt	960
415	Val	Tyr	Thr	Asp	Pro	Ile	Val	Phe	Asn	Arg	Glu	Thr	Ser	Gly	Gly	Phe	
416	305					310					315					320	
418	tgt	agg	cgt	tgg	tca	ctt	aac	agt	gat	att	tct	ttt	tca	gaa	gtc	gaa	1008
419	Cys	Arg	Arg	Trp	Ser	Leu	Asn	Ser	Asp	Ile	Ser	Phe	Ser	Glu	Val	Glu	
420					325					330					335		
422	agc	gct	gta	att	cgt	tca	cca	cac	cta	ttt	gat	ata	ctc	agt	gaa	ata	1056
423	Ser	Ala	Val	Ile	Arg	Ser	Pro	His	Leu	Phe	Asp	Ile	Leu	Ser	Glu	Ile	

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